



SEQUENCE LISTING

<110> SOCIETY

<120> GLUCOSE DEHYDROGENASE BETA-SUBUNIT AND
DNA ENCODING THE SAME

<130> TOYA126.002APC

<140> 10/511,796

<141> 2004-10-19

<150> PCT/JP03/05375

<151> 2003-04-25

<150> JP 2002-125353

<151> 2002-04-26

<160> 19

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2467

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (258)...(761)

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<222> (764)...(2380)

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<222> (2386)...(2466)

<400> 1

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tacgaatggc tgacacattg aatggactat aaaaccattg tccgttcggg aatgtgcgcg 180
tacatttcag gtccgcgccc atttttgaga aatatcaagc gtggttttcc cgaatccggt 240
gttcgagaga aggaaac atg cac aac gac aac act ccc cac tcg cgt cgc 290
                Met His Asn Asp Asn Thr Pro His Ser Arg Arg
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His Gly Asp Ala Ala Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln
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Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile			
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ggc gag cgc ctg ctg cag gcg ctg cag aag ggc tcg ttc aag acg gcc			530
Gly Glu Arg Leu Leu Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala			
	80	85	90
gac agc ctg ccg cag ctc gcc ggc gcg ctc gcg tcc ggt tcg ctg acg			578
Asp Ser Leu Pro Gln Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr			
	95	100	105
cct gaa cag gaa tcg ctc gca ctg acg atc ctc gag gcc tgg tat ctc			626
Pro Glu Gln Glu Ser Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu			
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ggc atc gtc gac aac gtc gtg att acg tac gag gaa gca tta atg ttc			674
Gly Ile Val Asp Asn Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe			
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ggc gtc gtg tcc gat acg ctc gtg atc cgt tcg tat tgc ccc aac aaa			722
Gly Val Val Ser Asp Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys			
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Pro Gly Phe Trp Ala Asp Lys Pro Ile Glu Arg Gln Ala Met Ala			
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Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser Gly Val			
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Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys Ala Val			
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Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile Val Glu			
	205	210	215
cgc ttc cgc aat cag ccc gac aag atg gac ttc atg gcg ccg tac ccg			961
Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro Tyr Pro			
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tcg agc ccc tgg gcg ccg cat ccc gag tac ggc ccg ccg aac gac tac			1009
Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn Asp Tyr			
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ctg atc ctg aag ggc gag cac aag ttc aac tcg cag tac atc cgc gcg			1057
Leu Ile Leu Lys Gly Glu His Lys Phe Asn Ser Gln Tyr Ile Arg Ala			
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gtg ggc ggc acg acg tgg cac tgg gcc gcg tcg gcg tgg cgc ttc att			1105
Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg Phe Ile			
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Pro Ile Gln Tyr Asp Asp Leu Glu Pro Tyr Tyr Gln Arg Ala Glu Glu	
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Glu Leu Gly Val Trp Gly Pro Gly Pro Glu Glu Asp Leu Tyr Ser Pro	
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Arg Lys Gln Pro Tyr Pro Met Pro Pro Leu Pro Leu Ser Phe Asn Glu	
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Gln Thr Ile Lys Thr Ala Leu Asn Asn Tyr Asp Pro Lys Phe His Val	
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Val Thr Glu Pro Val Ala Arg Asn Ser Arg Pro Tyr Asp Gly Arg Pro	
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act tgt tgc ggc aac aac aac tgc atg ccg atc tgc ccg atc ggc gcg	1441
Thr Cys Cys Gly Asn Asn Asn Cys Met Pro Ile Cys Pro Ile Gly Ala	
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atg tac aac ggc atc gtg cac gtc gag aag gcc gaa cgc gcc ggc gcg	1489
Met Tyr Asn Gly Ile Val His Val Glu Lys Ala Glu Arg Ala Gly Ala	
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Lys Leu Ile Glu Asn Ala Val Val Tyr Lys Leu Glu Thr Gly Pro Asp	
415 420 425	
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Lys Arg Ile Val Ala Ala Leu Tyr Lys Asp Lys Thr Gly Ala Glu His	
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Arg Val Glu Gly Lys Tyr Phe Val Leu Ala Ala Asn Gly Ile Glu Thr	
445 450 455	
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Pro Lys Ile Leu Leu Met Ser Ala Asn Arg Asp Phe Pro Asn Gly Val	
460 465 470	
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Ala Asn Ser Ser Asp Met Val Gly Arg Asn Leu Met Asp His Pro Gly	
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acc ggc gtg tcg ttc tat gcg agc gag aag ctg tgg ccg ggc cgc ggc	1777
Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly	
495 500 505	

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Ala	Thr	Glu	Ala	Ala	Lys	Lys	Ile	His	Leu	Ser	Asn	Leu	Ser	Arg	Ile	
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Phe	Asp	Cys	Phe	His	Glu	Ile	Leu	Pro	Gln	Pro	Glu	Asn	Arg	Ile	Val	
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Thr	Tyr	Ala	Ile	Asp	Asp	Tyr	Val	Lys	Arg	Gly	Ala	Ala	His	Thr	Arg	
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Glu	Val	Tyr	Ala	Thr	Ala	Ala	Lys	Val	Leu	Gly	Gly	Thr	Asp	Val	Val	
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ttc	aac	gac	gaa	ttc	gcg	ccg	aac	aat	cac	atc	acg	ggc	tcg	acg	atc	2209
Phe	Asn	Asp	Glu	Phe	Ala	Pro	Asn	Asn	His	Ile	Thr	Gly	Ser	Thr	Ile	
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atg	ggc	gcc	gat	gcg	cgc	gac	tcc	gtc	gtc	gac	aag	gac	tgc	cgc	acg	2257
Met	Gly	Ala	Asp	Ala	Arg	Asp	Ser	Val	Val	Asp	Lys	Asp	Cys	Arg	Thr	
				655					660					665		
ttc	gac	cat	ccg	aac	ctg	ttc	att	tcg	agc	agc	gcg	acg	atg	ccg	acc	2305
Phe	Asp	His	Pro	Asn	Leu	Phe	Ile	Ser	Ser	Ser	Ala	Thr	Met	Pro	Thr	
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gtc	ggg	acc	gta	aac	gtg	acg	ctg	acg	atc	gcc	gcg	ctc	gcg	ctg	cgg	2353
Val	Gly	Thr	Val	Asn	Val	Thr	Leu	Thr	Ile	Ala	Ala	Leu	Ala	Leu	Arg	
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Met	Ser	Asp	Thr	Leu	Lys	Lys	Glu	Val		Val	Arg	Lys	Ser	Thr	Leu	
	700					705						710				
act	ttc	ctc	atc	gcc	ggc	tgc	ctc	gcg	ttg	ccg	ggc	ttc	gcg	cgc	gcg	2451
Thr	Phe	Leu	Ile	Ala	Gly	Cys	Leu	Ala	Leu	Pro	Gly	Phe	Ala	Arg	Ala	
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gcc	gat	gcg	gcc	gat	c											2467

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<212> PRT
<213> Burkholderia cepacia

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35 40 45
Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser
50 55 60
Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu
65 70 75 80
Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln
85 90 95
Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser
100 105 110
Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn
115 120 125
Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe Gly Val Val Ser Asp
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<213> Burkholderia cepacia

<400> 3
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35 40 45
Val Glu Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro
50 55 60
Tyr Pro Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn
65 70 75 80
Asp Tyr Leu Ile Leu Lys Gly Glu His Lys Phe Asn Ser Gln Tyr Ile
85 90 95
Arg Ala Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg
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Phe Ile Pro Asn Asp Phe Lys Met Lys Ser Val Tyr Gly Val Gly Arg
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Ser	Pro	Arg	Lys	Gln	Pro	Tyr	Pro	Met	Pro	Pro	Leu	Pro	Leu	Ser	Phe
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Asn	Glu	Gln	Thr	Ile	Lys	Thr	Ala	Leu	Asn	Asn	Tyr	Asp	Pro	Lys	Phe
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His	Val	Val	Thr	Glu	Pro	Val	Ala	Arg	Asn	Ser	Arg	Pro	Tyr	Asp	Gly
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Gly	Ala	Lys	Leu	Ile	Glu	Asn	Ala	Val	Val	Tyr	Lys	Leu	Glu	Thr	Gly
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Pro	Asp	Lys	Arg	Ile	Val	Ala	Ala	Leu	Tyr	Lys	Asp	Lys	Thr	Gly	Ala
			260					265					270		
Glu	His	Arg	Val	Glu	Gly	Lys	Tyr	Phe	Val	Leu	Ala	Ala	Asn	Gly	Ile
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Glu	Thr	Pro	Lys	Ile	Leu	Leu	Met	Ser	Ala	Asn	Arg	Asp	Phe	Pro	Asn
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Pro	Gly	Thr	Gly	Val	Ser	Phe	Tyr	Ala	Ser	Glu	Lys	Leu	Trp	Pro	Gly
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Arg	Gly	Pro	Gln	Glu	Met	Thr	Ser	Leu	Ile	Gly	Phe	Arg	Asp	Gly	Pro
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Phe	Arg	Ala	Thr	Glu	Ala	Ala	Lys	Lys	Ile	His	Leu	Ser	Asn	Leu	Ser
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	370					375					380				
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Val	Gln	Phe	Asp	Cys	Phe	His	Glu	Ile	Leu	Pro	Gln	Pro	Glu	Asn	Arg
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Ile	Val	Pro	Ser	Lys	Thr	Ala	Thr	Asp	Ala	Ile	Gly	Ile	Pro	Arg	Pro
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Glu	Ile	Thr	Tyr	Ala	Ile	Asp	Asp	Tyr	Val	Lys	Arg	Gly	Ala	Ala	His
	435					440						445			
Thr	Arg	Glu	Val	Tyr	Ala	Thr	Ala	Ala	Lys	Val	Leu	Gly	Gly	Thr	Asp
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Thr	Ile	Met	Gly	Ala	Asp	Ala	Arg	Asp	Ser	Val	Val	Asp	Lys	Asp	Cys
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Arg	Thr	Phe	Asp	His	Pro	Asn	Leu	Phe	Ile	Ser	Ser	Ser	Ala	Thr	Met
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Pro	Thr	Val	Gly	Thr	Val	Asn	Val	Thr	Leu	Thr	Ile	Ala	Ala	Leu	Ala
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<212> PRT

<213> Burkholderia cepacia

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<210> 5
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial sequence; primer

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<210> 6
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial sequence; primer

<400> 6
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<210> 7
<211> 27
<212> DNA
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<220>
<223> Artificial sequence; primer

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<210> 8
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<223> Artificial sequence; primer

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<212> PRT
<213> Burkholderia cepacia

<400> 9

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1 5 10 15

<210> 10

<211> 25

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence; consensus

<221> UNSURE

<222> (6)...(6)

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<210> 11

<211> 2410

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (673)...(1950)

<400> 11

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cacgttcgac catccgaacc tgttcctctc gagcagctcg acgatgccga ccgtcggtac 600
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Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys
1 5 10

ctc gcg ctg ccc ggc ctc gca cgc gcg gcc gat tcg gcc gat ccg gcg	759
Leu Ala Leu Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala	
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cat gtc aag cgc ggc gaa tac ctc gcc gtc gcg ggc gac tgc atg gca	807
His Val Lys Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala	
30 35 40 45	
tgc cac acc gcg aag ggc ggc aag ccg ttc gcg ggc ggc ctc ggc atg	855
Cys His Thr Ala Lys Gly Gly Lys Pro Phe Ala Gly Gly Leu Gly Met	
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ccg gtg ccg atg ctc ggc aag atc tat acg agc aac atc aca ccg gat	903
Pro Val Pro Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp	
65 70 75	
ccc gat acc ggc atc ggc aac tgg acg ttc gag gac ttc gag cgc gcg	951
Pro Asp Thr Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala	
80 85 90	
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Val Arg His Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met	
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Pro Tyr Val Ser Tyr Ala Lys Ile Asn Asp Asp Asp Val Gln Ala Leu	
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Tyr Ala Tyr Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro	
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Lys Asn Glu Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile	
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Trp Asn Trp Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu	
160 165 170	
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Gln Ser Ala Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala	
175 180 185	
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His Cys Ser Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys	
190 195 200 205	
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Ser Leu Asp Glu Thr Gly Gly Ser Phe Leu Ser Gly Ser Val Leu Ala	
210 215 220	
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Gly Trp Asp Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly	
225 230 235	
ggc tgg acg cag cag cag ctc gtc cag tac ctg cgc acc ggc agc gtg	1431

Gly	Trp	Thr	Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	
		240					245					250				
ccg	ggc	ctc	gcg	cag	gcg	gcc	ggc	ccg	atg	gcc	gag	gcg	atc	gag	cac	1479
Pro	Gly	Leu	Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu	His	
	255					260				265						
agc	ttc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	ggc	ccg	atg	gcc	gag	1527
Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Gly	Pro	Met	Ala	Gly	
270					275				280						285	
gcg	atc	gag	cac	agc	ttc	tcg	aag	atg	acc	gaa	gcc	gac	atc	ggc	cgc	1575
Ala	Ile	Glu	His	Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Arg	
				290					295					300		
tcg	tcg	tgg	ggc	aag	ccg	gcc	gag	gat	ggc	ctg	aag	ctg	cgc	ggc	gtc	1623
Ser	Ser	Trp	Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	
			305					310					315			
gcg	ctc	gcg	tcg	tcg	ggc	atc	gat	ccg	gca	ccg	ctg	tat	ctc	ggc	aac	1671
Ala	Leu	Ala	Ser	Ser	Gly	Ile	Asp	Pro	Ala	Pro	Leu	Tyr	Leu	Gly	Asn	
		320					325					330				
tgc	gcg	acc	tgc	cac	cag	atg	cag	ggc	aag	ggc	acg	ccg	gac	ggc	tac	1719
Cys	Ala	Thr	Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	
	335					340				345						
tac	ccg	ccg	ttg	ttc	cac	aac	tcg	acg	gtc	ggc	gcg	tcg	aac	ccg	acc	1767
Tyr	Pro	Pro	Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Thr	
350					355					360					365	
aac	ctc	gtg	cag	gtg	atc	ctg	aac	ggc	gtg	cag	cgc	aag	gcc	ggc	agc	1815
Asn	Leu	Val	Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ala	Gly	Ser	
				370				375						380		
gag	gac	gtc	ggg	atg	ccc	gcg	ttc	cgc	cac	gag	ctg	tcg	gat	gcg	cag	1863
Glu	Asp	Val	Gly	Met	Pro	Ala	Phe	Arg	His	Glu	Leu	Ser	Asp	Ala	Gln	
			385					390					395			
atc	gcc	gcg	ctg	acg	aac	tac	ctg	acg	ggg	cag	ttc	ggc	aac	ccg	gcc	1911
Ile	Ala	Ala	Leu	Thr	Asn	Tyr	Leu	Thr	Gly	Gln	Phe	Gly	Asn	Pro	Ala	
		400					405					410				
gcg	aag	gtg	acc	gag	cag	gac	gtc	gcg	aag	ctg	cgc	tga	aacgcggcac			1960
Ala	Lys	Val	Thr	Glu	Gln	Asp	Val	Ala	Lys	Leu	Arg	*				
	415					420					425					
gcggcgaggc	agggcaacaa	tagaaaagag	gaggagcaca	gcacatcggg	cgggccccga											2020
tgccggttgt	tgacagcgcg	gacgggcggc	gcaggcggtc	gcccgtcctg	gttcacaggc											2080
aatccggtgc	gcgcacgcgc	cgcacgtgtt	tcgttgatcg	agaccatgac	accgaaccaa											2140
ccgtttctcg	cgtcccagcg	cgatgtgctg	ctgctgctgt	ccgaatacct	gctcgtgatc											2200
ctgttcgtga	tgttcggctg	gaagaagatt	atcgacttct	ccggtacgat	cgcgttcatg											2260
ggcagcgagg	gcgcgcgggc	gccgatcatc	tcggcggcga	tctccgtcgt	gatggagctc											2320
atcgtcggga	ttgcgatcct	cgtcggtttc	cagacgcggc	cgctcgcgct	gttgcttgcg											2380
ctgtacacga	tcggtaccgg	catcatcggc														2410

<210> 12

<211> 425
 <212> PRT
 <213> Burkholderia cepacia

<400> 12

Val	Arg	Lys	Ser	Thr	Leu	Thr	Phe	Leu	Leu	Ala	Gly	Cys	Leu	Ala	Leu
1			5					10					15		
Pro	Gly	Leu	Ala	Arg	Ala	Ala	Asp	Ser	Ala	Asp	Pro	Ala	His	Val	Lys
		20					25					30			
Arg	Gly	Glu	Tyr	Leu	Ala	Val	Ala	Gly	Asp	Cys	Met	Ala	Cys	His	Thr
	35						40					45			
Ala	Lys	Gly	Gly	Lys	Pro	Phe	Ala	Gly	Gly	Leu	Gly	Met	Pro	Val	Pro
	50					55					60				
Met	Leu	Gly	Lys	Ile	Tyr	Thr	Ser	Asn	Ile	Thr	Pro	Asp	Pro	Asp	Thr
65				70						75					80
Gly	Ile	Gly	Asn	Trp	Thr	Phe	Glu	Asp	Phe	Glu	Arg	Ala	Val	Arg	His
			85						90					95	
Gly	Val	Ser	Lys	Asn	Gly	Asp	Asn	Leu	Tyr	Pro	Ala	Met	Pro	Tyr	Val
			100					105					110		
Ser	Tyr	Ala	Lys	Ile	Asn	Asp	Asp	Asp	Val	Gln	Ala	Leu	Tyr	Ala	Tyr
		115				120						125			
Phe	Met	His	Gly	Val	Glu	Pro	Val	Lys	Gln	Ala	Pro	Pro	Lys	Asn	Glu
	130					135					140				
Ile	Pro	Ala	Leu	Leu	Ser	Met	Arg	Trp	Pro	Leu	Lys	Ile	Trp	Asn	Trp
145					150					155					160
Leu	Phe	Leu	Lys	Asp	Gly	Val	Tyr	Gln	Pro	Lys	Pro	Glu	Gln	Ser	Ala
			165						170					175	
Glu	Trp	Asn	Arg	Gly	Ala	Tyr	Leu	Val	Gln	Gly	Leu	Ala	His	Cys	Ser
			180					185					190		
Thr	Cys	His	Thr	Pro	Arg	Gly	Ile	Ala	Met	Gln	Glu	Lys	Ser	Leu	Asp
	195					200						205			
Glu	Thr	Gly	Gly	Ser	Phe	Leu	Ser	Gly	Ser	Val	Leu	Ala	Gly	Trp	Asp
	210					215					220				
Gly	Tyr	Asn	Ile	Thr	Ser	Asp	Pro	Asn	Ala	Gly	Ile	Gly	Gly	Trp	Thr
225					230					235					240
Gln	Gln	Gln	Leu	Val	Gln	Tyr	Leu	Arg	Thr	Gly	Ser	Val	Pro	Gly	Leu
			245						250					255	
Ala	Gln	Ala	Ala	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu	His	Ser	Phe	Ser
			260					265					270		
Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Gly	Pro	Met	Ala	Glu	Ala	Ile	Glu
		275				280						285			
His	Ser	Phe	Ser	Lys	Met	Thr	Glu	Ala	Asp	Ile	Gly	Arg	Ser	Ser	Trp
	290					295					300				
Gly	Lys	Pro	Ala	Glu	Asp	Gly	Leu	Lys	Leu	Arg	Gly	Val	Ala	Leu	Ala
305					310					315					320
Ser	Ser	Gly	Ile	Asp	Pro	Ala	Pro	Leu	Tyr	Leu	Gly	Asn	Cys	Ala	Thr
			325						330					335	
Cys	His	Gln	Met	Gln	Gly	Lys	Gly	Thr	Pro	Asp	Gly	Tyr	Tyr	Pro	Pro
			340					345					350		
Leu	Phe	His	Asn	Ser	Thr	Val	Gly	Ala	Ser	Asn	Pro	Thr	Asn	Leu	Val
		355					360						365		
Gln	Val	Ile	Leu	Asn	Gly	Val	Gln	Arg	Lys	Ala	Gly	Ser	Glu	Asp	Val
	370					375					380				
Gly	Met	Pro	Ala	Phe	Arg	His	Glu	Leu	Ser	Asp	Ala	Gln	Ile	Ala	Ala
385					390					395					400
Leu	Thr	Asn	Tyr	Leu	Thr	Gly	Gln	Phe	Gly	Asn	Pro	Ala	Ala	Lys	Val
				405					410					415	

Thr Glu Gln Asp Val Ala Lys Leu Arg
 420 425

<210> 13
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial sequence; primer

<400> 13
 tgcaccgtgc ggaaatctac tctcact 27

<210> 14
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificial sequence; primer

<400> 14
 atttccttct tcagcgtgtc cgacatc 27

<210> 15
 <211> 1441
 <212> DNA
 <213> Burkholderia cepacia

<220>
 <221> CDS
 <222> (121)...(1398)

<400> 15
 tccgaacctg ttcatttcga gcagcgcgac gatgccgacc gtcggtaccg taaacgtgac 60
 gctgacgata gccgcgctcg cgctgcggat gtcggacacg ctgaagaagg aagtctgacc 120
 gtg cgg aaa tct act ctc act ttc ctc atc gcc ggc tgc ctc gcg ttg 168
 Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
 1 5 10 15
 ccg ggc ttc gcg cgc gcg gcc gat gcg gcc gat ccg gcg ctg gtc aag 216
 Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys
 20 25 30
 cgc ggc gaa tac ctc gcg acc gcc atg ccg gta ccg atg ctc ggc aag 264
 Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys
 35 40 45
 atc tac acg agc aac atc acg ccc gat ccc gat acg ggc gac tgc atg 312
 Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met
 50 55 60
 gcc tgc cac acc gtg aag ggc ggc aag ccg tac gcg ggc ggc ctt ggc 360
 Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly
 65 70 75 80

ggc atc ggc aaa tgg acg ttc gag gac ttc gag cgc gcg gtg cgg cac	408
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His	
85 90 95	
ggc gtg tcg aag aac ggc gac aac ctg tat ccg gcg atg ccg tac gtg	456
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val	
100 105 110	
tcg tac gcg aag atc aag gac gac gac gta cgc gcg ctg tac gcc tac	504
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr	
115 120 125	
ttc atg cac ggc gtc gag ccg gtc aag cag gcg ccg ccg aag aac gag	552
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu	
130 135 140	
atc cca gcg ctg cta agc atg cgc tgg ccg ctg aag atc tgg aac tgg	600
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp	
145 150 155 160	
ctg ttc ctg aag gac ggc ccg tac cag ccg aag ccg tcg cag agc gcc	648
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala	
165 170 175	
gaa tgg aat cgc ggc gcg tat ctg gtg cag ggt ctc gcg cac tgc agc	696
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser	
180 185 190	
acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag tcg ctc gac	744
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp	
195 200 205	
gaa acc ggc ggc agc ttc ctc gcg ggg tcg gtg ctc gcc ggc tgg gac	792
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp	
210 215 220	
ggc tac aac atc acg tcg gac ccg aat gcg ggg atc ggc agc tgg acg	840
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr	
225 230 235 240	
cag cag cag ctc gtg cag tat ttg cgc acc ggc agc gtg ccg ggc gtc	888
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val	
245 250 255	
gcg cag gcg gcc ggg ccg atg gcc gag gcg gtc gag cac agc ttc tcg	936
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser	
260 265 270	
aag atg acc gaa gcg gac atc ggt gcg atc gcc acg tac gtc cgc acg	984
Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr	
275 280 285	
gtg ccg gcc gtt gcc gac agc aac gcg aag cag ccg cgg tcg tcg tgg	1032
Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp	
290 295 300	

ggc aag ccg gcc gag gac ggg ctg aag ctg cgc ggt gtc gcg ctc gcg 1080
 Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala
 305 310 315 320
 tcg tcg ggc atc gat ccg gcg cgg ctg tat ctc ggc aac tgc gcg acg 1128
 Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr
 325 330 335
 tgc cac cag atg cag ggc aag ggc acg ccg gac ggc tat tac ccg tcg 1176
 Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser
 340 345 350
 ctg ttc cac aac tcc acc gtc ggc gcg tcg aat ccg tcg aac ctc gtg 1224
 Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val
 355 360 365
 cag gtg atc ctg aac ggc gtg cag cgc aag atc ggc agc gag gat atc 1272
 Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile
 370 375 380
 ggg atg ccc gct ttc cgc tac gat ctg aac gac gcg cag atc gcc gcg 1320
 Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala
 385 390 395 400
 ctg acg aac tac gtg acc gcg cag ttc ggc aat ccg gcg gcg aag gtg 1368
 Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val
 405 410 415
 acg gag cag gac gtc gcg aag ctg cgc tga catagtcggg cgcgccgaca 1418
 Thr Glu Gln Asp Val Ala Lys Leu Arg *
 420 425
 cggcgcgaacc gataggacag gag 1441

<210> 16
 <211> 425
 <212> PRT
 <213> Burkholderia cepacia

<400> 16
 Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
 1 5 10 15
 Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys
 20 25 30
 Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys
 35 40 45
 Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met
 50 55 60
 Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly
 65 70 75 80
 Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
 85 90 95
 Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
 100 105 110
 Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr
 115 120 125
 Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu

130		135		140
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp				
145		150		155
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala				160
		165		170
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser				175
		180		185
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp				190
		195		200
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp				205
		210		215
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr				220
		225		230
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val				235
		245		250
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser				255
		260		265
Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr				270
		275		280
Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp				285
		290		295
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala				300
		305		310
Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr				315
		325		330
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser				335
		340		345
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val				350
		355		360
Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile				365
		370		375
Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala				380
		385		390
Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val				395
		405		410
Thr Glu Gln Asp Val Ala Lys Leu Arg				415
		420		425

<210> 17

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Artificial sequence; heme binding motif

<221> UNSURE

<222> (2)...(3)

<223> Xaa=unknown

<400> 17

Cys Xaa Xaa Cys His

1

5

<210> 18

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial sequence; primer

<400> 18
catgccatgg cacacaacga caacact

27

<210> 19
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial sequence; primer

<400> 19
cccaagcttg ggtcagactt ccttcttcag c

31